

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2004, 10:27:03 ; Search time 387 Seconds

(without alignments)
498.380 Million cell updates/sec

Title: US-09-701-747a-2

Perfect score: 2892
Sequence: 1 MPRIIVCKIKFAEDAKPKK.....LPNHHHPPGPGSLFENFAC 539

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PC1US_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2811	97.2	539	US-09-772-180A-8	Sequence 8, Appli
2	2811	97.2	539	US-10-295-027-290	Sequence 20, App
3	2799	96.8	539	US-09-772-180A-2	Sequence 2, Appli
4	2571	88.9	587	US-09-772-180A-4	Sequence 4, Appli
5	1275	44.1	526	US-09-983-204-13	Sequence 13, Appli
6	1261	43.6	514	US-10-092-900A-104	Sequence 104, App
7	1236	42.7	574	US-10-789-241-18	Sequence 18, Appli
8	1236	42.7	574	US-10-757-262-134	Sequence 14, App
9	1198	41.4	533	US-10-258-073-8	Sequence 8, Appli
10	1179	40.8	512	US-09-983-204-14	Sequence 14, Appli
11	1179	40.8	512	US-10-258-073-2	Sequence 2, Appli
12	1179	40.8	512	US-10-258-073-6	Sequence 6, Appli
13	1179	40.8	512	US-10-757-262-122	Sequence 122, App

14	1170	40.5	531	14	US-10-258-073-4	Sequence 4, Appli
15	1155.5	40.3	531	14	US-10-345-680-56	Sequence 56, Appli
16	1165.5	40.3	531	14	US-10-366-288-44	Sequence 44, Appli
17	1165.5	40.3	549	9	US-09-983-204-6	Sequence 6, Appli
18	1165	40.3	543	9	US-09-983-204-2	Sequence 2, Appli
19	1139.5	39.4	518	9	US-09-983-204-4	Sequence 4, Appli
20	510	17.6	150	9	US-09-860-670-108	Sequence 108, App
21	510	17.6	150	14	US-10-227-646-108	Sequence 108, App
22	466	16.1	103	10	US-09-772-180A-6	Sequence 6, Appli
23	416	14.4	704	14	US-10-104-047-3501	Sequence 3501, Ap
24	413	14.3	669	9	US-09-983-204-15	Sequence 15, Appli
25	413	14.3	669	13	US-10-133-157-4	Sequence 4, Appli
26	413	14.3	669	13	US-10-097-340-278	Sequence 278, App
27	413	14.3	669	14	US-10-097-340-280	Sequence 280, App
28	413	14.3	669	15	US-10-373-801-28	Sequence 28, Appli
29	413	14.3	669	15	US-10-133-573-4	Sequence 4, Appli
30	413	14.3	669	16	US-10-741-601-466	Sequence 466, App
31	410	14.2	638	9	US-09-983-204-18	Sequence 18, Appli
32	410	14.2	638	13	US-10-133-157-8	Sequence 8, Appli
33	410	14.2	638	15	US-10-133-573-8	Sequence 8, Appli
34	401.5	13.9	640	13	US-10-133-157-5	Sequence 5, Appli
35	401.5	13.9	640	15	US-10-133-573-5	Sequence 5, Appli
36	397.5	13.7	640	9	US-09-983-204-16	Sequence 16, Appli
37	362	12.5	649	13	US-10-133-573-6	Sequence 6, Appli
38	362	12.5	649	15	US-10-133-573-6	Sequence 6, Appli
39	349	12.1	649	9	US-09-983-204-17	Sequence 17, Appli
40	316	10.9	515	9	US-09-983-204-19	Sequence 19, Appli
41	287	9.9	374	14	US-10-104-047-3578	Sequence 3578, Ap
42	252	8.7	555	14	US-10-168-651-27	Sequence 27, Appli
43	229.5	7.9	907	14	US-10-369-493-6677	Sequence 6677, Ap
44	176.5	6.1	114	14	US-10-106-698-6921	Sequence 6921, Ap
45	155.5	5.4	46	15	US-10-276-774-1604	Sequence 1604, Ap

ALIGNMENTS

RESULT 1
US-09-772-180A-8
Sequence 8, Application US/09772180A
Publication No. US20030027749A1
GENERAL INFORMATION:
APPLICANT: David C. Harrison
APPLICANT: John Davis
APPLICANT: Sharon Bingham
APPLICANT: Trudy R. Doe
APPLICANT: Simon Topp
TITLE OR INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30021-C1
CURRENT APPLICATION NUMBER: US/09/772,180A
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: 09/063,848
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 9708936.1
PRIOR FILING DATE: 1997-05-01
PRIOR APPLICATION NUMBER: 97310289.0
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 9803566.0
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 539
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-772-180A-8
Query Match 97.2%; Score 2811; DB 10; Length 539;
Best Local Similarity 97.0%; Pred. No. 2.4e-258;
Matches 523; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
1 MPRIIVCKIKFAEDAKPKKADDEOSLGAAGAPAPDLPATFATSTLHGGRACP 60
|||||

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OM protein - protein search, using sw model

Run on: December 21, 2004, 09:55:38 ; Search time 24 Seconds
(without alignments)
1489.392 Million cell updates/sec

Title: US-09-701-747A-2
Perfect score: 2992
Sequence: 1 MPLEIVCKIKFAEDAKPKR.....LPNHHPHGGPGSLFENFAC 539

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgm2_6/ptodata/1/1aa/5A_COMB.pep:*
3: /cgm2_6/ptodata/1/1aa/5B_COMB.pep:*
4: /cgm2_6/ptodata/1/1aa/6A_COMB.pep:*
5: /cgm2_6/ptodata/1/1aa/6B_COMB.pep:*
6: /cgm2_6/ptodata/1/1aa/PCYUS_COMB.pep:*
7: /cgm2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2814	97.3	539	US-09-518-959-9	Sequence 9, Appli
2	2811	97.2	539	US-09-518-959-8	Sequence 8, Appli
3	1323	45.7	559	US-09-360-197-8	Sequence 8, Appli
4	1275	44.1	526	US-09-360-197-2	Sequence 2, Appli
5	1249.5	43.2	514	US-09-360-197-4	Sequence 4, Appli
6	1198	41.4	533	US-09-360-197-10	Sequence 10, Appli
7	1179	40.8	512	US-08-828-596-2	Sequence 2, Appli
8	1179	40.8	512	US-09-360-197-6	Sequence 6, Appli
9	1165.5	40.3	531	US-09-360-197-14	Sequence 14, Appli
10	1132.5	39.2	563	US-09-360-197-12	Sequence 12, Appli
11	413	14.3	702	US-09-917-254-94	Sequence 94, Appli
12	409.5	14.2	564	US-09-360-197-16	Sequence 16, Appli
13	409	14.1	698	US-08-376-362A-20	Sequence 20, Appli
14	408.5	14.1	625	US-09-360-197-15	Sequence 15, Appli
15	350	12.1	753	US-07-861-458C-98	Sequence 98, Appli
16	347	12.0	493	US-07-861-458C-98	Sequence 98, Appli
17	330	11.4	755	US-07-861-458C-99	Sequence 99, Appli
18	317.5	11.0	520	US-07-861-458C-100	Sequence 100, Appli
19	225.5	7.8	294	US-07-861-458C-100	Sequence 100, Appli
20	135	4.7	97	US-09-518-959-9	Sequence 9, Appli
21	132.5	4.2	173	US-09-518-959-9	Sequence 9, Appli
22	116.5	4.0	67	US-09-518-959-9	Sequence 9, Appli
23	113	3.9	1596	US-09-518-959-9	Sequence 9, Appli
24	110.5	3.8	1495	US-09-518-959-9	Sequence 9, Appli
25	110.5	3.8	1495	US-09-518-959-9	Sequence 9, Appli
26	105.5	3.6	830	US-09-518-959-9	Sequence 9, Appli
27	105.5	3.6	4545	US-08-804-227C-14	Sequence 14, Appli

28	105.5	3.6	4550	US-08-804-227C-8	Sequence 8, Appli
29	105.5	3.6	4550	US-08-804-198-2	Sequence 2, Appli
30	104.5	3.6	561	US-09-252-991A-16726	Sequence 16726, A
31	103	3.6	3729	US-08-804-227C-4	Sequence 4, Appli
32	98.5	3.4	830	US-09-562-737-32	Sequence 32, Appli
33	98.5	3.4	1841	US-08-804-227C-6	Sequence 6, Appli
34	98.5	3.4	4630	US-09-091-609-2	Sequence 2, Appli
35	98.5	3.4	5215	US-09-105-537-2	Sequence 2, Appli
36	98	3.4	671	US-09-252-991A-19375	Sequence 19375, A
37	97.5	3.4	11877	US-09-105-537-6	Sequence 6, Appli
38	95	3.3	40	US-07-861-458C-118	Sequence 118, Appli
39	94.5	3.3	830	US-09-562-737-31	Sequence 31, Appli
40	93	3.2	404	US-09-252-991A-21555	Sequence 21555, A
41	92.5	3.2	326	US-09-270-767-43738	Sequence 43738, A
42	92.5	3.2	1096	US-09-252-991A-19328	Sequence 19328, A
43	92	3.2	73	US-09-518-959-9	Sequence 9, Appli
44	92	3.2	885	US-08-312-892-4	Sequence 4, Appli
45	92	3.2	885	US-09-919-497-52	Sequence 52, Appli

ALIGNMENTS

RESULT 1					
US-09-518-959-9					
Sequence 9, Application US/09518959					
Patent No. 6548270					
GENERAL INFORMATION:					
APPLICANT: Dublin, Adrienne E					
APPLICANT: Huvar, Rene					
APPLICANT: Pyati, Jayashree					
TITLE OF INVENTION: DNA encoding human acid-sensing ion					
FILE REFERENCE: CRT-1197					
CURRENT APPLICATION NUMBER: US/09/518,959					
CURRENT FILING DATE: 2000-03-03					
NUMBER OF SEQ ID NOS: 9					
SOFTWARE: Patentm Ver. 2.1					
SEQ ID NO: 9					
LENGTH: 539					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-09-518-959-9					
Query Match					
Best Local Similarity 97.0%; Pred. No. 2.3e-284;					
Matches 523; Conservative 6; Mismatches 10; Indels 0; Gaps 0;					
QY	1	MPLEIVCKIKFAEDAKPKRKEAGDEOSLIGAAQAPAPDLPATFSTSLHIGRACGP	60		
DB	1	MPLEIVCKIKFAEDAKPKRKEAGDEOSLIGAAQAPAPDLPATFSTSLHIGRACGP	60		
QY	61	GPHELRRTLVALLSLAFLVQASLARGYLTRPHLVMDPAAPVAGPAPVTLTNT	120		
DB	61	GPHELRRTLVALLSLAFLVQASLARGYLTRPHLVMDPAAPVAGPAPVTLTNT	120		
QY	121	NRFFSLSDADIFHLNLTGLPKDGRRAAGLRPEEDMDVILNRTGHLADMLKSC	180		
DB	121	NRFFSLSDADIFHLNLTGLPKDGRRAAGLRPEEDMDVILNRTGHLADMLKSC	180		
QY	121	NRFFSLSDADIFHLNLTGLPKDGRRAAGLRPEEDMDVILNRTGHLADMLKSC	180		
DB	121	NRFFSLSDADIFHLNLTGLPKDGRRAAGLRPEEDMDVILNRTGHLADMLKSC	180		
QY	181	NFSGHCASNSFVYTRGKCTTFNADPOSSLPSRAAGSGLEIMLDTIQOEYLPIMR	240		
DB	181	NFSGHCASNSFVYTRGKCTTFNADPOSSLPSRAAGSGLEIMLDTIQOEYLPIMR	240		
QY	181	NFSGHCASNSFVYTRGKCTTFNADPOSSLPSRAAGSGLEIMLDTIQOEYLPIMR	240		
DB	181	NFSGHCASNSFVYTRGKCTTFNADPOSSLPSRAAGSGLEIMLDTIQOEYLPIMR	240		
QY	241	ETNETSEAGIRIQIHSGEPPYTHOIGFVSGFOTFVSCORLTYLPQPGNCRAES	300		
DB	241	ETNETSEAGIRIQIHSGEPPYTHOIGFVSGFOTFVSCORLTYLPQPGNCRAES	300		
QY	301	KLEPELQGSASVSACRLRCEKAVLQRCRMVMPENETICPPNITIECADHTLDS	360		
DB	301	KLEPELQGSASVSACRLRCEKAVLQRCRMVMPENETICPPNITIECADHTLDS	360		

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OM protein - protein search, using sw model

Run on: December 21, 2004, 09:47:03 ; Search time 23 Seconds
(without alignments)
2254.819 Million cell updates/sec

Title: US-09-701-747a-2

Perfect score: 2892
Sequence: 1 MPLEIVCKIKFAEDAKPKK.....LPNHHHPGPGSLFENFAC 539

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	1142.5	39.5	532	2 JE0091	testis sodium chan
2	422.5	14.6	548	2 T25401	hypothetical prote
3	413	14.3	669	2 A49585	Nat channel protei
4	410	14.2	638	2 T19156	amiloride sensitiv
5	408.5	14.1	625	2 S68434	PKRfamily-activat
6	405	14.0	699	2 S29499	sodium channel pro
7	402.5	13.9	640	2 T51915	epithelial sodium
8	397.5	13.7	650	2 A51065	sodium transport p
9	396.5	13.7	632	2 T51682	epithelial sodium
10	390.5	13.5	664	2 T20420	hypothetical prote
11	386.5	13.4	660	2 T51684	epithelial sodium
12	383	13.2	663	2 T25569	hypothetical prote
13	381.5	13.2	724	2 T25700	mechanosensory pro
14	368.5	12.7	545	2 T25429	hypothetical prote
15	363.5	12.6	638	2 S41159	sodium transport p
16	361	12.5	649	2 T64847	epithelial sodium
17	356	12.3	795	2 T34468	hypothetical prote
18	354.5	12.3	849	2 T19878	hypothetical prote
19	354.5	12.3	926	2 H88226	protein C41C4.5 [i
20	349	12.1	648	2 T38204	epithelial amilor
21	347	12.0	749	2 T29859	mechanosensory pro
22	331.5	11.5	629	2 T25571	hypothetical prote
23	329	11.4	737	2 T16737	hypothetical prote
24	327.5	11.3	638	2 T37309	f1r-1 protein - Ca
25	319.5	11.0	630	2 D87739	hypothetical prote
26	319.5	11.0	630	2 T25144	hypothetical prote
27	314	10.9	608	2 T25572	hypothetical prote
28	308	10.7	643	2 T21296	hypothetical prote
29	307.5	10.6	613	2 T28952	hypothetical prote

30	269.5	9.3	611	2 T20501	hypothetical prote
31	264	9.1	978	2 T16948	hypothetical prote
32	236.5	8.2	297	2 T25652	degenerin 1 (DEG-1
33	230	8.0	599	2 T15552	hypothetical prote
34	229.5	7.9	907	2 T27317	hypothetical prote
35	203	7.0	292	2 T29233	hypothetical prote
36	190.5	6.6	606	2 T20054	amiloride-sensitiv
37	160	5.5	384	2 T19513	hypothetical prote
38	154.5	5.3	840	2 T21333	hypothetical prote
39	113	3.9	1596	2 A35927	190K DNA-binding p
40	110.5	3.8	1495	2 S80255	transcription co-r
41	104.5	3.6	956	2 B83200	probable phosphotr
42	104.5	3.6	6260	2 T30228	polyketide synthas
43	103	3.6	1535	2 S46224	peroxidasein - fru
44	101.5	3.5	1207	1 EGHU	epidermal growth f
45	99.5	3.4	1400	1 T38185	protein-tyrosine k

ALIGNMENTS

RESULT 1
JE0091
testis sodium channel 1 - human
C/Species: Homo sapiens (man)
C/Date: 14-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: JE0091
R/hibashi, K.; Marumo, F.
Biochem. Biophys. Res. Commun. 245, 589-593, 1998
A/Title: Molecular cloning of a DEG/ENac sodium channel cDNA from human testis.
A/Reference number: JE0091, M0ID:98238685, PMID:9571199
A/Accession: JE0091
A/Molecule type: mRNA
A/Residues: 1-532 <ISH>
A/Cross-references: UNIPROT:O60263; DDBJ:AB010575; NID:G3097313; PIDN:BA25897.1; PID:G:
A/Experimental source: testis
C/Keywords: glycoprotein; mitochondrion
F/43-61,443-462/Region: hydrophobic
F/175/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	39.5%	Score 1142.5	DB 2	Length 532
Best Local Similarity	45.9%	Pred. No. 2.3e-85		
Matches 247	Conservative 62	Mismatches 172	Indels 57	Gaps 12
QY	35	GPAAPR-----DLATPASTSTHGLGRACGPGPRGLRRTLVALLTSLAFLQAASLAR	90	
DB	6	GPEBARQASDIRVFASNCMGLGVFGFGLSLRGMMAAVLVSATFLVQVARRVR	65	
QY	91	GYLTRPHTLVMDPAAPAPVAGPPAVTLGNINFRHSALSPADIFHLAN--LTGLPPQRD	148	
DB	66	YNEFHQRLDLDBESHRLL-PPAVTLGNINPLRRRLTPNDL-HWAGSLGLDPAEHA	123	
QY	149	GHRDAGLRPEP-----DWDVILNRTGQLOLADMLKSCNFGHCSANFSVYTRY	199	
DB	124	APFLAALGRPPAPPGFMPSPFFDMAQLYARAGSLDMLDCCRFGQPCGPEMTTITFTM	183	
QY	200	GKCYTN--ADPOSSLPSRAGWGSGLEIMLDIOEELVPIKBTNETSPFAGIRQIHS	257	
DB	184	GKCYTRSGADGAEILLTTRGGMGNGJDMVDVQGSYLPVWMDNEETPEVGIQVQIHG	243	
QY	258	QEEPPYIHQIFGVSPGFQTFVSCOEORLTLYLPQPMNGCRAS-----K	301	
DB	244	HEBPPIIDQGLGVSPGYQTFVSCQGOQLSLFPPPGDSSALNINYEBSPLGSPK	303	
QY	302	LREPELGYSAYSVAACRLCEKEAVLQRCHEVMVMPGNETICPNYITECDHTLDSL	361	
DB	304	PPAPAL-----PIPMGCRLACETRYVYARKCGCMVMPGVPVPCSPQOXYGCAHPADAM	359	
QY	362	GGSGEPPCPPTPCNTLRYSKEISWTKIPNBSGARLYARKNNENYIEENPLVLVPFE	421	
DB	360	--LRKSCAPNCASTRYAKELSMVRIPSRAARFLARKNRRBAYIAENVLALDIFFE	417	
QY	422	ALTSEAMEGRAPAYGSLALGLDGLGQMLPFGASITLTLEILDYEVSWDR-LKRVWRP	480	

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OM protein - protein search, using sw model

Run on: December 21, 2004, 07:56:27 ; Search time 73 Seconds
(without alignments)
2648.700 Million cell updates/sec

Title: US-09-701-747a-2

Perfect score: 2892
Sequence: 1 MPLEIVCKIKFAEDAKPKR.....LPNHHKPPGSLFENFAC 539

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2892	100.0	539	AAV53870	AAY53870 Amino aci
2	2814	97.3	539	AAE10898	AAE10898 Human bra
3	2811	97.2	539	AAW80318	AAW80318 Neurodege
4	2811	97.2	539	AAE10897	AAE10897 Human bra
5	2811	97.2	539	ABR58577	ABR58577 Human can
6	2811	97.2	539	ADN38972	ADN38972 Cancer/an
7	2811	97.2	653	ABP69359	ABP69359 Human pol
8	2799	96.8	539	AAW80315	AAW80315 Neurodege
9	2571	88.9	587	AAW80316	AAW80316 Neurodege
10	1897	65.6	401	AAW07750	AAW07750 A human a
11	1323	45.7	559	AAW68507	AAW68507 Rat aci
12	1323	45.7	559	AAV69178	AAV69178 A rat aci
13	1311.5	45.3	562	ABP70739	ABP70739 Human pro
14	1296	44.8	513	AAV03186	AAV03186 Rat Acid
15	1275	44.1	526	AAW68504	AAW68504 Rat aci
16	1275	44.1	526	AAV03188	AAV03188 Rat Acid
17	1275	44.1	526	AAV69175	AAV69175 A rat aci
18	1265	43.7	318	ADH22534	ADH22534 Human tra
19	1261	43.6	514	ABU65092	ABU65092 Human NOV
20	1249.5	43.2	514	ADN61835	ADN61835 Human nov
21	1249.5	43.2	514	AAW68505	AAW68505 Human aci
22	1249.5	43.2	514	AAV69176	AAV69176 A partial
23	1198	41.4	533	AAW68508	AAW68508 Rat aci
24	1198	41.4	533	AAV69179	AAV69179 A rat aci
25	1198	41.4	533	AAU10906	AAU10906 Rat aci

26	1198	41.4	533	8	ADN97426	ADN97426 Rat DRASI
27	1179	40.8	512	2	AAW68506	AAW68506 Human aci
28	1179	40.8	512	2	AAW93420	AAW93420 Human BNC
29	1179	40.8	512	3	AAV69177	AAV69177 A human a
30	1179	40.8	512	5	AAU10905	AAU10905 Rat aci
31	1179	40.8	512	5	AAU10903	AAU10903 Human aci
32	1179	40.8	512	7	ADN14073	ADN14073 Human src
33	1179	40.8	512	8	ADK71115	ADK71115 Human aci
34	1179	40.8	512	8	ADN97420	ADN97420 Rat BNC1
35	1179	40.8	512	8	ADP43821	ADP43821 Human aci
36	1170	40.5	531	2	AAV09509	AAV09509 Human pro
37	1170	40.5	531	5	AAU10904	AAU10904 Human aci
38	1170	40.5	531	8	ADN97424	ADN97424 Human DRA
39	1165.5	40.3	529	8	ADQ28595	ADQ28595 Human SLN
40	1165.5	40.3	531	3	AAV69181	AAV69181 A human a
41	1165.5	40.3	531	7	AAE38601	AAE38601 Human aci
42	1165.5	40.3	531	7	ADE30465	ADE30465 Human aci
43	1165.5	40.3	549	2	AAW68252	AAW68252 Sodium ch
44	1165	40.3	543	2	AAW88250	AAW88250 Sodium ch
45	1139.5	39.4	518	2	AAW88251	AAW88251 Sodium ch

ALIGNMENTS

RESULT 1
AAV53870
ID AAV53870 standard; protein; 539 AA.

AC AAV53870;

DT 13-MAR-2000 (first entry)

XX Amino acid sequence of a H+-gated cation channel designated SPASIC.

XX H+-gated cation channel; SPASIC; dorsal root ganglion; gene therapy;

XX acid sensitive cation channel; central nervous system; pain response;

XX ion channel activity; neurotransmitter release; analgesic;

XX neuromodulatory; anti-inflammatory; neurotransmitter release;

XX neuronal excitability.

OS Rattus norvegicus.

XX W09963081-A2.

XX 09-DEC-1999.

PF 03-JUN-1999; 99WO-GB001743.

XX 03-JUN-1998; 98GB-00011965.

PA (UNLO) UNIV COLLEGE LONDON.

XX Wood JN, England S, Chen CC, Akopian AN;

XX WPI; 2000-086977/07.

DR N-PSDB; AA236802.

PT Novel ion channel protein for use as an analgesic drug target and for

XX identifying novel analgesic and antiinflammatory agents.

XX Claim 2; Page 51-52; 55pp; English.

PS The present sequence represents a H+-gated cation channel, designated

CC SPASIC. The CDNA sequence was isolated from a rat dorsal root ganglion

CC cDNA library. The protein is an acid sensitive cation channel capable of

CC reversibly mediating rapid and sustained cation current. The channel is

CC present in dorsal root ganglion and in central nervous system tissues.

CC The SPASIC polynucleotide and polypeptide are used in influencing

CC electrophysiological and/or pharmacological properties of a cell.

CC Expression of the SPASIC gene or antisense sequences leads to an increase

CC or reduction in ion channel activity. The SPASIC gene is used in gene

CC therapy or in preparation of medicaments for gene therapy to inhibit pain

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:28:07 ; Search time 1710 Seconds

(without alignment)
8465.284 Million cell updates/sec

Title: US-09-701-747A-1

Perfect score: 2622
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4093002 seqs, 2760418825 residues

Word size : 16

Total number of hits satisfying chosen parameters: 297542

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	80	3.1	2431	16	US-10-302-172-458
2	80	3.1	2710	15	US-10-295-027-289
3	80	3.1	2711	10	US-09-772-180A-1
4	80	3.1	2955	10	US-09-772-180A-1
5	80	2.6	462	10	US-09-918-995-481
6	68	2.6	465	10	US-09-918-995-481
7	68	2.6	1632	10	US-09-772-180A-7
8	40	1.5	65	10	US-09-908-975-2131
9	30	1.1	424	11	US-09-969-034-1620
10	29	1.1	254	16	US-10-424-599-84829
11	29	1.1	396	9	US-09-825-294-20
12	29	1.1	396	9	US-09-970-966-20

C 13	29	1.1	396	10	US-09-814-353-4322	Sequence 4322, Ap
C 14	29	1.1	396	10	US-09-814-353-10626	Sequence 10626, A
C 15	29	1.1	396	15	US-10-212-677-20	Sequence 20, Appl
C 16	29	1.1	396	15	US-10-361-811-20	Sequence 20, Appl
C 17	29	1.1	396	15	US-10-369-186-20	Sequence 20, Appl
C 18	29	1.1	451	9	US-09-860-670-39	Sequence 39, Appl
C 19	29	1.1	451	15	US-10-227-646-39	Sequence 39, Appl
C 20	29	1.1	462	15	US-10-101-510-176	Sequence 176, App
C 21	29	1.1	462	15	US-10-101-510-176	Sequence 176, App
C 22	29	1.1	574	9	US-09-919-580-71	Sequence 71, Appl
C 23	29	1.1	613	11	US-09-969-034-828	Sequence 828, App
C 24	29	1.1	891	14	US-10-198-846-6156	Sequence 6156, Ap
C 25	29	1.1	1374	17	US-10-437-963-84556	Sequence 84556, A
C 26	29	1.1	1654	18	US-10-425-115-44120	Sequence 44120, A
C 27	28	1.1	39	15	US-10-219-195-28	Sequence 28, Appl
C 28	28	1.1	39	15	US-10-219-195-28	Sequence 28, Appl
C 29	28	1.1	39	15	US-10-219-195-34	Sequence 34, Appl
C 30	28	1.1	39	15	US-10-219-195-49	Sequence 49, Appl
C 31	28	1.1	41	11	US-09-876-143-867	Sequence 867, App
C 32	28	1.1	46	9	US-09-827-289-22	Sequence 22, Appl
C 33	28	1.1	46	9	US-09-827-289-26	Sequence 26, Appl
C 34	28	1.1	62	16	US-10-182-327-182	Sequence 182, App
C 35	28	1.1	64	9	US-09-983-965-42	Sequence 42, Appl
C 36	28	1.1	67	9	US-09-983-965-245	Sequence 245, App
C 37	28	1.1	70	9	US-09-925-298-396	Sequence 396, App
C 38	28	1.1	70	14	US-10-102-806-396	Sequence 396, App
C 39	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 40	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 41	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 42	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 43	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 44	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 45	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 46	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
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C 83	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 84	28	1.1	75	11	US-09-876-143-867	Sequence 867, App
C 85	28	1.1	75	11	US-09-876-143-867	Sequence 867, App

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 03:58:12 / Search time 151 Seconds

(without alignments) 12342.308 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	68	2.6	1620	4	US-09-518-959-6
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5	31	1.2	40	4	US-09-518-959-5
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8	29	1.1	396	4	US-09-825-294-20
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11	28	1.1	46	4	US-09-827-289-22
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13	28	1.1	54	2	US-08-776-944-8
14	28	1.1	55	4	US-09-621-976-11651
15	28	1.1	57	4	US-09-513-999C-19821
16	28	1.1	59	4	US-09-621-976-11876
17	28	1.1	69	4	US-09-621-976-11887
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22	28	1.1	77	4	US-09-621-976-12266
23	28	1.1	81	3	US-09-014-416-57
24	28	1.1	81	4	US-09-621-976-12198
25	28	1.1	81	4	US-09-621-976-13601
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56	1.1	149	4	US-09-621-976-8863	Sequence 8863, Ap
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67	1.1	164	4	US-09-621-976-8070	Sequence 8070, Ap
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73	1.1	182	4	US-09-621-976-16234	Sequence 16234, A
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92	1.1	249	4	US-09-621-976-13322	Sequence 13322, Ap
93	1.1	253	2	US-08-520-678A-25	Sequence 25, Appl1
94	1.1	253	2	US-08-897-126-25	Sequence 25, Appl1
95	1.1	257	2	US-08-520-678A-24	Sequence 24, Appl1
96	1.1	257	2	US-08-897-126-24	Sequence 24, Appl1
97	1.1	260	2	US-08-520-678A-29	Sequence 29, Appl1
98	1.1	260	3	US-08-897-126-29	Sequence 29, Appl1
99	1.1	261	4	US-09-621-976-17067	Sequence 17067, A
100	1.1	267	4	US-09-621-976-14155	Sequence 14155, A

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 02:00:56 ; Search time 818 Seconds
(without alignments)
16826.384 Million cell updates/sec

Title: US-09-701-747A-1

Perfect score: 2622
Sequence: 1 agtgcacgcctgcgcggtgc.....aaaaaaaaaaaaaaaaaaaa 2622

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 16

Total number of hits satisfying chosen parameters: 249225

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : N_Geneseq_23Sep04:*

- 1: geneseq1980s:*
- 2: geneseq1990s:*
- 3: geneseq2000s:*
- 4: geneseq2001as:*
- 5: geneseq2001bs:*
- 6: geneseq2002as:*
- 7: geneseq2002bs:*
- 8: geneseq2003as:*
- 9: geneseq2003bs:*
- 10: geneseq2003cs:*
- 11: geneseq2003ds:*
- 12: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2622	100.0	2622	3 AA236802	AA236802 Nucleic a
2	80	3.1	2431	6 AB211576	AB211576 Human pol
3	80	3.1	2431	12 ADMA44094	ADMA44094 Novel hum
4	80	3.1	2516	3 AA559323	AA559323 DNA encod
5	80	3.1	2528	5 AA18265	AA18265 Human bra
6	80	3.1	2710	10 ACC72703	ACC72703 Human can
7	80	3.1	2710	11 ADN38971	ADN38971 Cancer/an
8	80	3.1	2711	2 AAV68056	AAV68056 Neurodege
9	80	3.1	2752	12 ADH22600	ADH22600 CDNA enco
10	80	3.1	2955	2 AAV68057	AAV68057 Neurodege
11	68	2.6	462	9 ACH13269	ACH13269 Human adu
12	68	2.6	465	9 ACH13266	ACH13266 Human adu
13	68	2.6	1203	3 AA559324	AA559324 Coding re
14	68	2.6	1632	2 AAV68059	AAV68059 Neurodege
15	40	1.5	65	6 ABN29383	ABN29383 Rat splic
16	32	1.2	50	5 AAD18260	AA18260 Human bra
17	31	1.2	40	5 AAD18264	AA18264 Oligo use
18	30	1.1	424	6 ABQ57925	ABQ57925 Human col
19	29	1.1	271	4 AAI14984	AA14984 Human bre
20	29	1.1	313	5 ABV04496	ABV04496 Human pro
21	29	1.1	335	5 ABV57836	ABV57836 Human pro

C 22	29	1.1	396	4 AAF94829	AAF94829 Human ova
C 23	29	1.1	396	5 ADL36736	ADL36736 Human ova
C 24	29	1.1	396	6 ADL71580	ADL71580 Human ova
C 25	29	1.1	396	6 ABL48779	ABL48779 Ovarian c
C 26	29	1.1	396	6 ABT03096	ABT03096 Human ova
C 27	29	1.1	396	11 ADM10689	ADM10689 Human ova
C 28	29	1.1	396	12 ADJ11019	ADJ11019 Represent
C 29	29	1.1	396	12 ADM43280	ADM43280 Human ova
C 30	29	1.1	451	4 AAI62780	AAI62780 Human CDN
C 31	29	1.1	451	5 ABA13241	ABA13241 Human ner
C 32	29	1.1	462	6 ABZ35505	ABZ35505 Human gen
C 33	29	1.1	462	6 ABZ35064	ABZ35064 Human gen
C 34	29	1.1	574	6 ABK54601	ABK54601 Human col
C 35	29	1.1	613	6 ABQ57133	ABQ57133 Human col
C 36	28	1.1	41	6 ABN73933	ABN73933 Bovine em
C 37	28	1.1	45	12 ADM98336	ADM98336 Human FGB
C 38	28	1.1	46	6 AAS95732	AAS95732 Allele di
C 39	28	1.1	46	6 AAS95736	AAS95736 Allele di
C 40	28	1.1	48	6 ABK30223	ABK30223 CYP2D6 ge
C 41	28	1.1	51	4 AAL30531	AAL30531 Human SNP
C 42	28	1.1	51	6 ABK30191	ABK30191 CYP2D6 ge
C 43	28	1.1	52	6 ABK30190	ABK30190 CYP2D6 ge
C 44	28	1.1	54	2 AAT17031	AAT17031 Human mit
C 45	28	1.1	55	12 ADM98347	ADM98347 Human LPL
C 46	28	1.1	57	3 AAC15746	AAC15746 Human sec
C 47	28	1.1	62	5 AAD13992	AAD13992 Deletion
C 48	28	1.1	64	8 ABX50113	ABX50113 Bovine BS
C 49	28	1.1	65	12 ADM98353	ADM98353 Human NPP
C 50	28	1.1	66	10 ADF11666	ADF11666 Human SRP
C 51	28	1.1	67	6 ABX14133	ABX14133 Fluorece
C 52	28	1.1	67	8 ABX50316	ABX50316 Bovine ES
C 53	28	1.1	70	3 AAF22009	AAF22009 Human bre
C 54	28	1.1	75	6 ABE73475	ABE73475 Bovine em
C 55	28	1.1	78	6 ABV96830	ABV96830 Human pan
C 56	28	1.1	83	3 AAF22006	AAF22006 Human pan
C 57	28	1.1	84	12 ADK52282	ADK52282 Murine ty
C 58	28	1.1	85	12 ADG55306	ADG55306 Template
C 59	28	1.1	87	6 ABA99435	ABA99435 B. mori T
C 60	28	1.1	89	8 ABA44974	ABA44974 Bovine BS
C 61	28	1.1	90	2 AAT47082	AAT47082 Synthetic
C 62	28	1.1	101	6 ABL37986	ABL37986 Human col
C 63	28	1.1	101	6 ADG19100	ADG19100 RNA-depen
C 64	28	1.1	103	10 ADC17856	ADC17856 Monobacta
C 65	28	1.1	107	10 ADC17845	ADC17845 Monobacta
C 66	28	1.1	108	4 AAH43640	AAH43640 SSG #6. 1
C 67	28	1.1	109	5 AAF98681	AAF98681 Human ova
C 68	28	1.1	109	8 ABX37401	ABX37401 Bovine ES
C 69	28	1.1	110	2 AAX35561	AAX35561 Secreted
C 70	28	1.1	110	9 ADA45152	ADA45152 Human pol
C 71	28	1.1	111	10 ADC17844	ADC17844 Monobacta
C 72	28	1.1	111	10 ADG37675	ADG37675 Aspergill
C 73	28	1.1	112	10 ADC17848	ADC17848 Monobacta
C 74	28	1.1	114	10 ADC17852	ADC17852 Monobacta
C 75	28	1.1	115	6 ABA82937	ABA82937 Human pro
C 76	28	1.1	116	6 AAL19706	AAL19706 Human bre
C 77	28	1.1	117	6 ABE97342	ABE97342 Human pan
C 78	28	1.1	120	3 AA889576	AA889576 Exo20 nuc
C 79	28	1.1	120	4 AAH70046	AAH70046 Human cer
C 80	28	1.1	120	6 ABE76458	ABE76458 Bacillus
C 81	28	1.1	121	8 ABE54306	ABE54306 Bovine ES
C 82	28	1.1	122	12 ADO41190	ADO41190 Human CDN
C 83	28	1.1	125	6 ABL37601	ABL37601 Human col
C 84	28	1.1	127	2 AAX24845	AAX24845 Infectio
C 85	28	1.1	130	4 AAK89973	AAK89973 Human dig
C 86	28	1.1	130	4 AAI62629	AAI62629 Human bre
C 87	28	1.1	130	4 AAK78760	AAK78760 Human lmm
C 88	28	1.1	130	4 AAK79573	AAK79573 Human lmm
C 89	28	1.1	130	4 AAK73943	AAK73943 Human lmm
C 90	28	1.1	130	4 AAL06723	AAL06723 Human rep
C 91	28	1.1	130	4 AAL05021	AAL05021 Human rep
C 92	28	1.1	130	4 AAL07126	AAL07126 Human rep
C 93	28	1.1	130	4 ABA08160	ABA08160 Human ova
C 94	28	1.1	130	4 ABL97914	ABL97914 Human tes

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 02:03:42 ; Search time 7228 Seconds

(without alignments)
17154.620 Million cell updates/sec

Title: US-09-701-747A-1

Perfect score: 2622
Sequence: 1 agtgcacgcgtctgcggtgc.....aaaaaaaaaaaaaaaaa 2622

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 2364489745 residues

Word size : 16

Total number of hits satisfying chosen parameters: 478857

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2622	100.0	2622	6 AX009297	Sequence
2	2195	83.7	2622	10 RNO242554	Rattus no
3	1761	67.2	2532	10 RNO271642	Au271642 Rattus no
4	823	31.4	216648	10 AC112361	AC112361 Rattus no
5	823	31.4	266167	2 AC121633	AC121633 Rattus no
6	161	6.1	2301	10 BC046481	BC046481 Mus muscu
7	161	6.1	2478	10 BC055772	BC055772 Mus muscu
8	137	5.2	177632	2 AC114651	AC114651 Mus muscu
9	137	5.2	197109	2 AC115011	AC115011 Mus muscu
10	80	3.1	2528	6 AR306271	AR306271 Sequence
11	80	3.1	744	9 HSA408881	HSA408881 Homo sapi
12	80	3.1	2697	6 AR306271	AR306271 Sequence
13	80	3.1	2711	6 E31843	E31843 Novel compo
14	80	3.1	2711	6 AX002412	AX002412 Sequence
15	80	3.1	2955	6 E31844	E31844 Novel compo
16	80	3.1	2955	6 AX002414	AX002414 Sequence
17	80	3.1	3345	9 BC031812	BC031812 Homo sapi
18	80	3.1	3685	9 HSA271643	AJ271643 Homo sapi
19	80	3.1	183625	9 AC053503	AC053503 Homo sapi

20	80	3.1	184176	2 AC149120	AC149120 Papio anu
21	80	3.1	186883	2 AC040991	AC040991 Homo sapi
22	80	3.1	193064	2 AC149860	AC149860 Papio anu
23	68	2.6	1620	6 AR306270	AR306270 Sequence
24	68	2.6	1632	6 E31846	E31846 Novel compo
25	68	2.6	1632	6 AX002418	AX002418 Sequence
26	68	2.6	2439	9 BC073912	BC073912 Homo sapi
27	63	2.4	200465	2 AC148786	AC148786 Otolenur
28	63	2.4	215101	2 AC148847	AC148847 Otolenur
29	59	2.3	1452	6 CQ714799	CQ714799 Sequence
30	50	1.9	1315	9 HSA408882	AJ408882 Homo sapi
31	31	1.9	135033	9 AC009955	AC009955 Homo sapi
32	42	1.6	53239	2 AC011971	AC011971 Homo sapi
33	33	1.5	65	6 CQ532496	CQ532496 Sequence
34	32	1.2	50	6 AR306265	AR306265 Sequence
35	35	1.2	40	6 AR306269	AR306269 Sequence
36	30	1.1	601	11 G94636	G94636 S208P6415RB
37	29	1.1	271	6 CQ422415	CQ422415 Sequence
38	29	1.1	313	6 CQ472620	CQ472620 Sequence
39	29	1.1	335	6 CQ525988	CQ525988 Sequence
40	29	1.1	336	6 CQ397251	CQ397251 Sequence
41	29	1.1	396	6 CQ403555	CQ403555 Sequence
42	29	1.1	396	6 AR391197	AR391197 Sequence
43	29	1.1	396	6 AR392902	AR392902 Sequence
44	29	1.1	396	6 AR489632	AR489632 Sequence
45	29	1.1	396	6 AR493873	AR493873 Sequence
46	29	1.1	396	6 AX093202	AX093202 Sequence
47	29	1.1	574	6 AX381133	AX381133 Sequence
48	29	1.1	1547	9 HSA408884	AJ408884 Homo sapi
49	29	1.1	183793	2 CR450793	CR450793 Danio rer
50	29	1.1	186883	2 AC040991	AC040991 Homo sapi
51	29	1.1	190260	2 CR538726	CR538726 Danio rer
52	29	1.1	227369	2 AC114469	AC114469 Rattus no
53	29	1.1	230637	2 AC095345	AC095345 Rattus no
54	29	1.1	246991	2 AC122956	AC122956 Rattus no
55	28	1.1	249173	2 AC135886	AC135886 Rattus no
56	28	1.1	44	6 AR038858	AR038858 Sequence
57	28	1.1	46	6 AX287579	AX287579 Sequence
58	28	1.1	46	6 AX287583	AX287583 Sequence
59	28	1.1	51	6 CQ005099	CQ005099 Sequence
60	28	1.1	54	6 A49113	A49113 Sequence 8
61	28	1.1	55	6 AR420154	AR420154 Sequence
62	28	1.1	55	6 AX980848	AX980848 Sequence
63	28	1.1	55	6 BD115707	BD115707 EST and e
64	28	1.1	57	6 AX903958	AX903958 Sequence
65	28	1.1	57	6 BD039491	BD039491 Sequence
66	28	1.1	59	6 AR420379	AR420379 Sequence
67	28	1.1	59	6 AX981073	AX981073 Sequence
68	28	1.1	59	6 BD115932	BD115932 EST and e
69	28	1.1	62	6 AX205290	AX205290 Sequence
70	28	1.1	69	6 AR420390	AR420390 Sequence
71	28	1.1	69	6 AR420957	AR420957 Sequence
72	28	1.1	69	6 AX981084	AX981084 Sequence
73	28	1.1	69	6 AX981651	AX981651 Sequence
74	28	1.1	69	6 BD115943	BD115943 EST and e
75	28	1.1	69	6 BD116510	BD116510 EST and e
76	28	1.1	70	6 AR420943	AR420943 Sequence
77	28	1.1	70	6 AX981637	AX981637 Sequence
78	28	1.1	70	6 BD116496	BD116496 EST and e
79	28	1.1	72	6 AR420893	AR420893 Sequence
80	28	1.1	72	6 AX981587	AX981587 Sequence
81	28	1.1	72	6 BD116446	BD116446 EST and e
82	28	1.1	73	6 AR423201	AR423201 Sequence
83	28	1.1	73	6 AX983895	AX983895 Sequence
84	28	1.1	73	6 BD118754	BD118754 EST and e
85	28	1.1	77	6 AR420769	AR420769 Sequence
86	28	1.1	77	6 AX981463	AX981463 Sequence
87	28	1.1	77	6 BD116322	BD116322 EST and e
88	28	1.1	81	6 AR119865	AR119865 Sequence
89	28	1.1	81	6 AR420701	AR420701 Sequence
90	28	1.1	81	6 AR422104	AR422104 Sequence
91	28	1.1	81	6 AX981395	AX981395 Sequence
92	28	1.1	81	6 AX982798	AX982798 Sequence

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 00:33:06 ; Search time 908 Seconds

(Without alignments)
15942.331 Million cell updates/sec

Title: US-09-701-747a-1

Perfect score: 2622
Sequence: 1 agcagacagcgtcgcgggtgc.....aaaaaaaaaaaaaaaaa 2622

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PTCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PTCT_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1834.2	70.0	2710	15	US-10-295-027-289
2	1816.6	69.3	2711	10	US-09-772-180A-1
3	1717	65.5	2431	16	US-10-302-172-458
4	1555	59.3	2955	10	US-09-772-180A-3
5	1411.2	53.8	1632	10	US-09-772-180A-7
6	463.8	17.7	1624	16	US-10-092-900A-103
7	391.4	14.9	1732	15	US-10-258-073-3
8	391.2	14.9	1596	15	US-10-345-680-57
9	391.2	14.9	1650	9	US-09-983-204-5
10	391.2	14.9	1723	9	US-09-983-204-1
11	391.2	14.9	1746	15	US-10-345-680-55
12	391.2	14.9	1746	15	US-10-366-288-43

Result No.	Score	Query Match	Length	DB ID	Description
13	387.6	14.8	1711	9	US-09-983-204-3
14	385	14.7	3918	15	US-10-101-510-421
15	385	14.7	3923	17	US-10-283-975A-64
16	385	14.7	3923	17	US-10-789-241-17
17	385	14.7	3923	18	US-10-757-262-133
18	351	13.4	1602	15	US-10-258-073-7
19	335	12.8	1539	9	US-09-954-456-750
20	335	12.8	1539	16	US-10-305-720-1102
21	335	12.8	1663	18	US-10-757-262-121
22	335	12.8	2555	15	US-10-258-073-5
23	335	12.8	2748	15	US-10-258-073-1
24	332.8	12.7	462	15	US-10-101-510-116
25	332.8	12.7	462	15	US-10-101-510-616
26	318.6	12.2	451	9	US-09-860-670-39
27	318.6	12.2	451	15	US-10-227-646-39
28	309.6	11.5	397	9	US-09-960-352-1490
29	300.6	11.5	465	10	US-09-918-995-478
30	299.4	11.4	462	10	US-09-918-995-481
31	263	10.0	508	10	US-09-772-180A-5
32	191.2	7.3	831	13	US-10-027-633-155396
33	191.2	7.3	831	15	US-10-027-633-155396
34	173.6	6.6	393	16	US-10-305-720-206
35	115.2	4.4	425	9	US-09-960-352-10001
36	114.2	4.4	458	10	US-09-918-995-28399
37	112.2	4.3	358	9	US-09-728-445-590
38	80.6	3.1	354	15	US-10-106-698-2644
39	75.8	2.9	438	16	US-10-276-774-254
40	64	2.4	65	10	US-09-908-975-2131
41	63.6	2.4	343	17	US-10-283-975A-116
42	50.8	1.9	459	10	US-09-918-995-2809
43	50	1.9	2931	13	US-10-027-633-111727
44	50	1.9	2931	15	US-10-027-633-111727
45	46.8	1.8	653	17	US-10-437-963-94593

ALIGNMENTS

RESULT 1
US-10-295-027-289
Sequence 289, Application US/10295027
Publication No. US2003022350A1
GENERAL INFORMATION:
APPLICANT: Ataz, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glyme, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 21:43:21 ; Search time 151 Seconds

(without alignments)
12342.308 Million cell updates/sec

Title: US-09-701-747A-1
Barfoot score: 3633

Sequence: 1 agtcgacagctgtgcggtgc.....aaaaaaaaaaaaa 2622

Scoring table: IDENTITY_NUC

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_NA:*

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1: /cg2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cg2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cg2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cg2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cg2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cg2_6/ptodata/1/ina/backfl1es1.seq:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1748	66.7	2528	4	US-09-518-959-7	Sequence 7, Appl11
2	1717	65.5	2431	4	US-09-799-451-458	Sequence 458, Appl1
3	1400.8	53.4	1620	4	US-09-518-959-6	Sequence 6, Appl1
4	491.2	18.7	3647	3	US-09-360-197-7	Sequence 7, Appl1
5	440.2	16.8	1620	3	US-09-360-197-3	Sequence 3, Appl1
6	415	15.8	3562	3	US-09-360-197-1	Sequence 1, Appl1
7	391.2	14.9	1736	3	US-09-360-197-13	Sequence 13, Appl1
8	351	13.4	1602	3	US-09-360-197-9	Sequence 9, Appl1
9	347.2	13.2	1948	3	US-09-360-197-11	Sequence 11, Appl1
10	335	12.8	1539	2	US-08-828-996-1	Sequence 1, Appl1
11	335	12.8	1539	4	US-09-016-434-1102	Sequence 1102, Appl1
12	335	12.8	1666	3	US-09-360-197-5	Sequence 5, Appl1
13	173.6	6.6	7218	1	US-09-016-434-206	Sequence 206, Appl1
14	47.8	1.8	7218	2	US-08-232-463-14	Sequence 14, Appl1
15	43.2	1.6	2218	2	US-08-845-998-5	Sequence 5, Appl1
16	43.2	1.6	2218	3	US-09-206-537-5	Sequence 5, Appl1
17	43.2	1.6	2218	3	US-09-430-854-5	Sequence 5, Appl1
18	42.8	1.6	1605	4	US-09-149-476-187	Sequence 187, Appl1
19	40.8	1.6	985	4	US-09-332-409-25	Sequence 25, Appl1
20	40.8	1.6	985	4	US-09-332-409-27	Sequence 27, Appl1
21	40.8	1.6	985	4	US-09-451-527-25	Sequence 25, Appl1
22	40.8	1.6	985	4	US-09-451-527-27	Sequence 27, Appl1
23	40.6	1.5	2639	3	US-09-374-135-1	Sequence 1, Appl1
24	40.6	1.5	7218	1	US-08-232-463-14	Sequence 14, Appl1
25	40.4	1.5	1988	2	US-08-712-948-8	Sequence 8, Appl1
26	40.4	1.5	1988	2	US-09-073-655-1218	Sequence 1218, Appl1
27	40	1.5	2255	2	US-08-845-998-3	Sequence 3, Appl1

28	40	1.5	2259	3	US-09-206-553-3	Sequence 3, Appl1	
C	29	40	1.5	2259	3	US-09-430-854-3	Sequence 3, Appl1
C	30	39.8	1.5	8051	2	US-08-576-628A-2	Sequence 2, Appl1
C	31	39.4	1.5	636	3	US-09-385-968-317	Sequence 317, Appl1
C	32	39.2	1.5	474	4	US-09-621-977-18033	Sequence 18033, A
C	32	39.2	1.5	1013	4	US-09-322-409-6	Sequence 6, Appl1
C	33	39.2	1.5	1013	4	US-09-322-409-6	Sequence 6, Appl1
C	34	39.2	1.5	1013	4	US-09-322-409-6	Sequence 6, Appl1
C	35	39.2	1.5	1013	4	US-09-451-527-6	Sequence 8, Appl1
C	36	39.2	1.5	1013	4	US-09-451-527-6	Sequence 8, Appl1
C	37	39	1.5	289	3	US-09-007-005-17	Sequence 17, Appl1
C	38	39	1.5	289	3	US-09-653-839-9	Sequence 9, Appl1
C	39	39	1.5	2806	4	US-09-244-796-17	Sequence 17, Appl1
C	40	39	1.5	2806	4	US-10-202-619-9	Sequence 9, Appl1
C	41	38.8	1.5	8100	4	US-09-554-337-4	Sequence 4, Appl1
C	42	38.8	1.5	11517	1	US-07-920-281C-1	Sequence 1, Appl1
C	43	38.8	1.5	11517	4	US-08-466-27-1	Sequence 1, Appl1
C	44	38.8	1.5	11517	4	US-09-688-84-1	Sequence 1, Appl1
C	45	38.8	1.5	15538	4	US-09-554-337-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1

; Sequence 7, Application US/09518959

GENERAL INFORMATION:

APPLICANT: Erlander, Mark G

APPLICANT: Pyati, Jayashree

TITLE OF INVENTION: channel BNaC4 (ASIC4)

CURRENT APPLICATION NUMBER: US/09/518,955

NUMBER OF SEQ ID NOS: 9

; SEQ ID NO 7

TYPE: DNA

US-09-518-959-7

Query Match	66.7%;	Score 1748;	DB 4;	Length 2528;
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Matches 2131; Conservative 0; Mismatches 353; Indels 49; Gaps 13;

Qy	120	AGCCCCCAACCTCGGGCCCCCAACCCCTGGTCCCATCTCTCTCTGATGGCCCTGAGTTAG	187
Db	1	ACTCCCCCACTCGGGCCCCCAACCCCTGGTCCCATCTCTCTCTGATGGCCCTGAGTTAG	60
Qy	188	AAGAGCAGCGCGTGGCCACCAACCACTCCGAGGGGACACAGGCTGCTGTCCAGGGAG	247
Db	61	AAGAGCAGCGCGTGGCCACCACTCGGAGGGACACAGGCTGCTGTGAGGAGG	122
Qy	248	GACAGTAGCAGTAGGGCTCTGGCCAGTCCCAAGCAAGCCGGGACAGATGCCATCGAGATT	307
Db	121	GACAG-GGAGGGAGGGCTCTGGCCAGTCCCAAGCAGCGGGACAGATGCCATCGAGATT	179
Qy	308	GTTGTGCAAAATCAATTTCGTGAGGAGATGCAAAACCAAGAGAAAGAGCAGGGAT	367
Db	180	GTTGTCAAAATCAAAATTTTGTGTGAGGAGATGCAAAACCAAGAGAAAGAGCAGGGAT	238
Qy	368	GAGCAGAGGCTCTGGGGGTGCTCAAGGGGCAAGAGCCCTCGGGACCTGGCTAACTTTT	427
Db	240	GAGCAGAGGCTCTCGGGGTGTTCGCCCTGAGAGAGGCCCTCCGAGACCTGGCCACTTT	299
Qy	428	GCCAGACCAAGTACTGTGATGGGCTGGAGCGGGCTTGGCCAGAGCCCCCATGATGACTG	487
Db	300	GCCAGACCAAGACCTGTGATGATCTGGAGCGGGCTTGTGGCCAGAGCCCCCATGAGACTG	355

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OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 21:31:31 ; Search time 5273 Seconds

(without alignments)
18119.662 Million cell updates/sec

Title: US-09-701-747A-1

Perfect score: 2622

Sequence: 1 agtgaacagctgcgcgggtgc.....aaaaaaaaaaaaaaaaa 2622

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	749.6	28.6	799	6	CA749777 UI-M-FD0-
2	743.6	28.4	825	4	BI731397 603353854
3	695.8	26.5	724	5	BQ442411 UI-M-EV0-
4	669.2	25.5	690	5	BU709210 UI-M-EV0-
5	646.8	24.7	703	4	BM386997 UI-R-CN1-
6	641.2	24.5	779	5	EX345391 BX345391
7	613.8	22.4	633	5	BU058742 UI-M-FR0-
8	589.2	22.5	658	2	BB621654 BB621654
9	520.2	19.8	679	1	AV323885 AV323885
10	478.6	18.3	585	6	CB058292 NISC_1x02
11	473	18.0	512	2	BR121356 UI-R-CN0-
12	463.4	17.7	740	4	BG911389 602807694
13	458.8	17.5	812	4	BG818664 602778855
14	453.8	17.3	464	2	BF565208 UI-R-B01-
15	437	16.7	473	2	BF411609 UI-R-BT1-
16	436.4	16.6	474	2	AM527475 UI-R-B01-
17	404.2	15.4	3830	3	BC028722 Homo sapi
18	401.4	15.3	513	4	BM257315 520890 MA
19	398	15.2	616	4	BG912088 602809988
20	390.4	14.9	451	5	BY290885 BY290885
21	381.8	14.6	426	5	BY295044 BY295044
22	380.2	14.5	1059	4	BG825318 602747771
23	372.6	14.2	940	1	AL534267 AL534267
24	372.4	14.2	405	6	CB810840 AMGNNUC:T

C	25	369.8	14.1	400	2	BF393596 UI-R-CA0-
	26	358.4	13.7	391	6	CB775482 AMGNNUC:T
	27	358.4	13.7	400	1	AL362900 AL362900
	28	357.6	13.6	450	6	CA451772 UI-M-FX0-
C	29	356.6	13.6	712	8	B2195341 CH230-465
	30	351.4	13.4	384	6	CB703338 AMGNNUC:T
	31	348.4	13.3	435	6	CB792852 AMGNNUC:T
	32	344	13.1	3470	3	HSW805478
C	33	335.8	12.8	759	9	AG353117 Mus muscu
	34	333.2	12.7	866	7	CK238032 AGENNCOURT
	35	329.2	12.6	423	2	AM669129 112310 MA
	36	325.8	12.4	433	6	BY652580 BY652580
	37	320.6	12.2	483	6	CA779219 MP1384.8
	38	317.6	12.1	667	4	BC912912 602807305
	39	315.4	12.0	451	6	CB787201 AMGNNUC:T
C	40	315.4	12.0	473	6	CB730080 AMGNNUC:N
	41	311	11.9	337	7	CR457643 CR457643
	42	298.8	11.4	708	4	BG913866 602812380
C	43	294.2	11.2	323	2	AM530335 UI-R-BU0-
	44	292.8	11.2	382	6	BY656489 BY656489
	45	274.2	10.5	1254	6	CD326863 AGENNCOURT

ALIGNMENTS

RESULT 1
LOCUS CA749777 799 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FD0-cdg-a-19-0-UI-r1 NIH BMAP_FDO Mus musculus cDNA clone
IMAGE:6828284 5', mRNA sequence.

CA749777
CA749777.1 GI:25572573
EST.
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS 1 (bases 1 to 799)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at:
http://image.llnl.gov

FEATURES
Seq primer: pyx-5
Location/Qualifiers
1..799
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6828284"
/feature_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (11.5 phage resistant)"
/note="Organ: Brain; Vector: pyx-asc; Site 1: Bcor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Bcor I adaptor, digested with Not I, and then

